Package ‘betafam’

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Author Wei Guo <wei.guo3@nih.gov>
Maintainer Wei Guo <wei.guo3@nih.gov>
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Description To detecting rare variants for quantitative traits using nuclear families, the linear combination methods are proposed using the estimated regression coefficients from the multiple regression and regularized regression as the weights.
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Description

To detecting rare variants for quantitative traits using nuclear families, the linear combination methods are proposed using the estimated regression coefficients from the multiple regression and regularized regression as the weights.
betafam

Usage

betafam(ped, group.threshold=-1, fix.group.index=NULL, fix.weight=NULL, mute.SMM=TRUE, trait=c("binary", "qtl"), LC.test=c("LC.true", "LC", "sig.LC", "LC.mreg", "LC.lasso", "LC.elasticnet"), sig.LC.cutoff=0, true.beta=NULL, ped2multifam=FALSE, useParInRegression=FALSE, trace=FALSE)

Arguments

ped input data, has same format with PLINK but having column names. The PED file is a white-space (space or tab) delimited file; the first six columns are mandatory: FID: Family ID; IID: Individual ID; FA: Paternal ID; MO: Maternal ID; SEX: Sex (1=male; 2=female; other=unknown); PHENO: Phenotype; Genotypes (column 7 onwards) should also be white-space delimited; they are coded as 0, 1 and 2, indicating the number of coding allele, and NA is for missing genotype.

group.threshold optional, indicates the minor allele frequency threshold that alleles will be grouped marker in the pre-group step before the linear combination test; default is -1, which means all markers are not grouped.

fix.group.index optional, indicates the fixed grouping index for each marker regardless of the group.threshold value. The length of this vector equals the number of markers. For example, if fix.group.index=c(1,1,2,2,2), the first two markers will be grouped and the last three will grouped together marker in the pre-group step. Default is NULL, which means no pre-group is to be done.

fix.weight optional, indicates the fixed weight for each marker in the pre-group step. The length of this vector equals the number of markers. Default is NULL, which means the weight on each marker is automatically specified by 1/sqrt(q(1-q)), where q is the minor allele frequency.

mute.SMM indicates whether or not the multi-marker test, same as FBAT -m test, should be calculated; default is TRUE.

trait taking values as c("binary", "qtl"), indicates the trait type, either binary ("binary") or quantitative ("qtl").

LC.test taking values as c("LC.true", "LC", "sig.LC", "LC.mreg", "LC.lasso", "LC.elasticnet"), indicates which test should be included in the linear combination methods. See details in the reference paper.

sig.LC.cutoff indicates the pvalue threshold for grouping the markers with pvalue< sig.LC.cutoff in the sig.LC test; default is 0.

true.beta indicates the true beta values used as the weights in the linear combination methods for simulation use only. Alternatively, this could be used as fixed weights given by the user.

ped2multifam indicates whether or not a pedigree could be separated into multiple nuclear families. Default is FALSE.

useParInRegression indicates whether or not parents will be used in the linear regression for estimating the weights. Default is FALSE.

trace indicates whether or not the intermediate outcomes should be printed; default is FALSE.
Value

- singleP: pvalues for the single marker tests.
- minP: minimum pvalue for the single marker tests.
- Z: test statistic Z=S-E(S).
- Z.stat: Z statistics for each marker or group.
- Zk.var: variance calculating by parental genotypes.
- allele.weight: frequency-determined weights.
- group.index: group index used in the pre-group step.
- Ngroup: number of groups in the pre-group step.
- sigma: empirical variance matrix.
- inv.sigma: inverse sigma.
- SMM.stat: multiple marker test statistic
- SMM.pvalue: pvalue on the multiple marker test.
- why.SMM.na: reason that the SMM test does not exist.
- LC.beta: estimated betas in the LC test based on the single marker regression.
- LC.stat: LC test statistic
- LC.pvalue: pvalue on the LC test
- sig.LC.beta: estimated betas in the sig.LC test.
- sig.LC.stat: sig.LC test statistic
- sig.LC.pvalue: pvalue on the sig.LC test
- true.LC.beta: estimated betas in the true.LC test.
- true.LC.stat: true.LC test statistic
- true.LC.pvalue: pvalue on the true.LC test
- mreg.LC.beta: estimated betas in the mreg.LC test.
- mreg.LC.stat: mreg.LC test statistic
- mreg.LC.pvalue: pvalue on the mreg.LC test
- lasso.LC.beta: estimated betas in the lasso.LC test.
- lasso.LC.stat: lasso.LC test statistic
- lasso.LC.pvalue: pvalue on the lasso.LC test
- elasticnet.LC.beta: estimated betas in the elasticnet.LC test.
- elasticnet.LC.stat: elasticnet.LC test statistic
- elasticnet.LC.pvalue: pvalue on the elasticnet.LC test
- runtime: runtime of this program.
- fam.info: nuclear families in the ped data.
References

Guo W, Shugart YY, Detecting Rare Variants for Quantitative Traits Using Nuclear Families (manuscript).

Examples

```r
# example.ped <- read.table("example.ped", head=1, stringsAsFactors=F)
# library(glmnet)
# test <- betaFam(ped=example.ped, trace=TRUE)
# test$elasticnet.LC.pvalue
```

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**call.moment**

*Calculating the expectation and variance of the offspring’s genotype conditional on parental genotypes.*

**Description**

The expectation and variance are calculated with respect to parental genotypes at a single marker under the null distribution of parental random transmission using Mendel’s laws.

**Usage**

```r
call.moment(father, mother)
```

**Arguments**

- `father` indicates the father’s genotype, coded as 0, 1 and 2.
- `mother` indicates the mother’s genotype, coded as 0, 1 and 2.

**Value**

- `mean` expectation of the offspring’s genotype.
- `var` variance of the offspring’s genotype.

**References**

Guo W, Shugart YY, Detecting Rare Variants for Quantitative Traits Using Nuclear Families (manuscript).

**Examples**

```r
call.moment(1,1)
```
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